## Amendments to the Specification

At page 14 of the specification, please amend the paragraph beginning at line 4 as follows:

"Homology" refers to the percent of identity between at least two oligonucleotides or polypeptides. The percent identity between the sequences from one moiety to another can be determined by techniques known in the art. Homology can be determined by a direct comparison of the sequence information between two polypeptide molecules by aligning the sequence information and using readily available computer programs such as ALIGN, Dayhoff, M.O. (1978) in *Atlas of Protein Sequence and Structure* 5:Supp. 3, National Biomedical Research Foundation, Washington, DC. Default parameters can be used for alignment. One alignment program is BLAST, used with default or manually set parameters. Details of these programs can be found, for example, on the website of the National Center for Biotechnology Information (NCBI). at the following Internet address: http://www.ncbi.nlm.gov/cgi-bin/BLAST.